



## Conserved Domain Database

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**CD: smart00087.10, PTH, Query added**
**PSSM-Id: 77**
**Source: Smart**
**Description:** Parathyroid hormone;

**Taxa:** [Amniota](#)
**References:** [1 Pubmed Link](#)
**Status:** Alignment from source

**Created:** 12-Dec-2003

**Aligned:** 6 rows

**PSSM:** 36 columns

**Representative:** Consensus

**Proteins:** [\[Click here for CDART summary of Proteins containing smart00087\]](#)
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width 60

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up to 10

sequences most similar to the query

```

                10      20      30
          .....*.....|.....*.....|.....*.....|.....*
consensus  1 KRAVSEHQLMHNLGKHIQDLERREWLRKKLQDVHTA 36
query      1 --SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN- 32
gi 131544  35 KRAVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIHNTA 70
gi 131541  36 KRAVSEHQLLHDKGKSIQDLRRRIFLQNLIEGVNTA 71
gi 131545  30 KRAVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHNF 65
gi 131546  30 KRSVSEMQLMHNLGHRHTVERQDWLQMKLQDVHSA 65
gi 131548  30 KRSVSEIQLMHNLGKHLSSLERVEWLRKKLQDVHNF 65

```

**Citing CDD:** Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen PA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, Bryant SH (2003), "CDD: a curated Entrez database of conserved domain alignments", *Nucleic Acids Res.* 31: 383-387

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changes  
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NEWS 10 MAR 29 WPIFV now available on STN  
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NEWS 12 APR 26 PROMT: New display field available  
NEWS 13 APR 26 IFIPAT/IFIUDB/IFICDB: New super search and display field  
available  
NEWS 14 APR 26 LITAlert now available on STN  
NEWS 15 APR 27 NLDB: New search and display fields available  
NEWS 16 May 10 PROUSDDR now available on STN  
NEWS 17 May 10 PROUSDDR: One FREE connect hour, per account, in both May  
and June 2004  
  
NEWS EXPRESS MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT  
MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),  
AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004  
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ENTRY	SESSION
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=> S cyclohexylalanine AND Cha AND pth2  
L1 0 CYCLOHEXYLALANINE AND CHA AND PTH2

=> S PTH AND cyclohexylalanine  
L2 0 PTH AND CYCLOHEXYLALANINE

=> S SVSEIQaHNAGKHLNSNERVEWLRKKLQDVHN  
L3 0 SVSEIQAHNAGKHLNSNERVEWLRKKLQDVHN

=> S SVSEIQ\*  
L4 0 SVSEIQ\*

=> S PTH2 RECEPTOR LIGAND  
L5 2 PTH2 RECEPTOR LIGAND

=> DUP REM  
ENTER L# LIST OR (END):L5  
PROCESSING COMPLETED FOR L5  
L6 1 DUP REM L5 (1 DUPLICATE REMOVED)

=> D

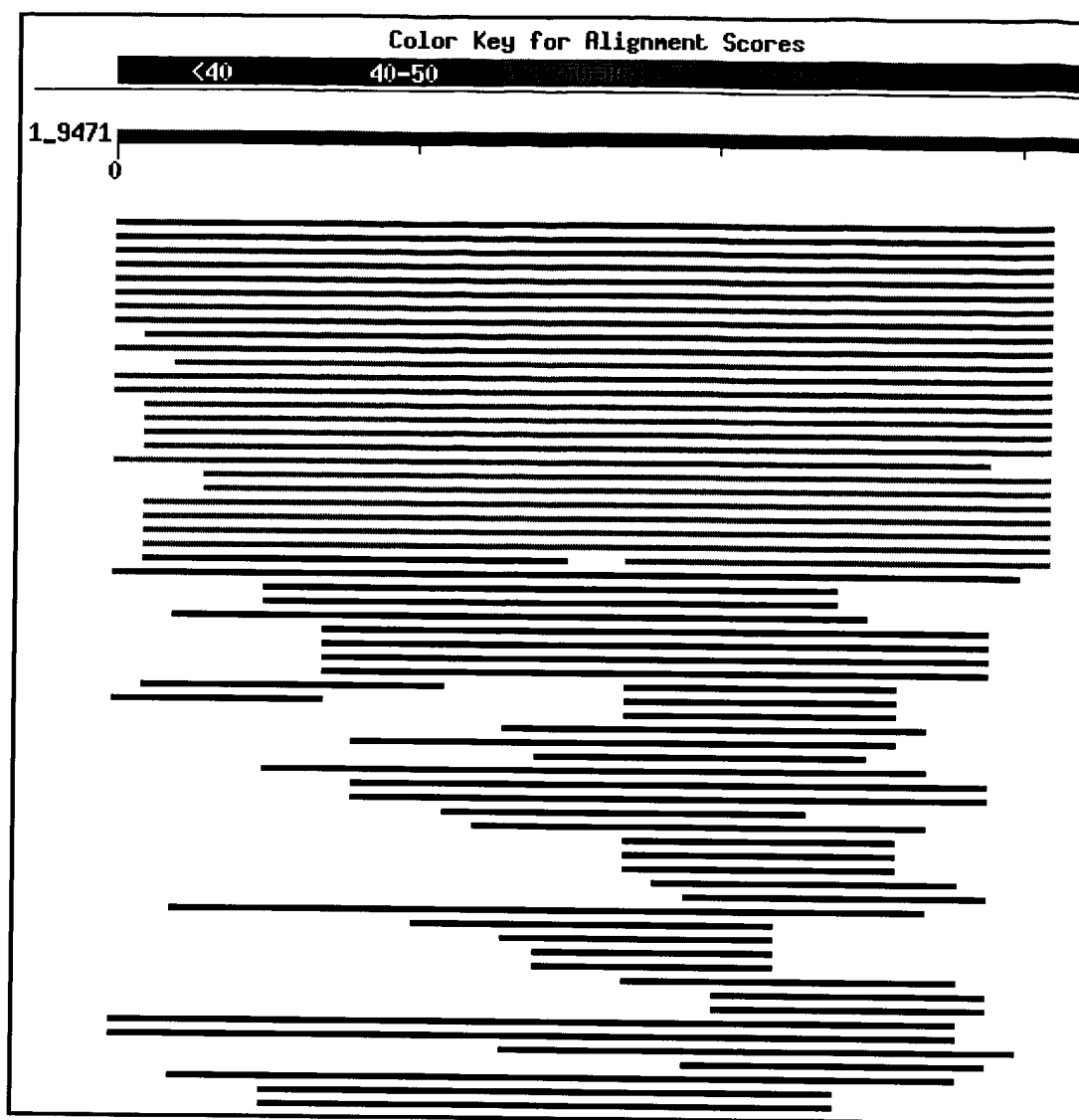
L6 ANSWER 1 OF 1 MEDLINE on STN DUPLICATE 1  
AN 1999427840 MEDLINE  
DN PubMed ID: 10499494  
TI Comparison of rat and human parathyroid hormone 2 (PTH2) receptor  
activation: PTH is a low potency partial agonist at the rat PTH2 receptor.  
AU Hoare S R; Bonner T I; Usdin T B  
CS Unit on Cell Biology, Laboratory of Genetics, National Institute of Mental  
Health, Bethesda, Maryland 20892-4094, USA.  
SO Endocrinology, (1999 Oct) 140 (10) 4419-25.  
Journal code: 0375040. ISSN: 0013-7227.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Abridged Index Medicus Journals; Priority Journals  
EM 199910  
ED Entered STN: 19991026  
Last Updated on STN: 19991026  
Entered Medline: 19991012

=> LOGOFF HOLD  
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
5.80	6.07

FULL ESTIMATED COST

SESSION WILL BE HELD FOR 60 MINUTES  
STN INTERNATIONAL SESSION SUSPENDED AT 15:37:51 ON 11 MAY 2004



### Related Structures

Sequences producing significant alignments:		Score	E
		(bits)	Value
<a href="#">gi 7416876 gb AAF62347.1 </a>	parathyroid hormone [Equus caballus]	85	1e-16
<a href="#">gi 13124462 sp Q9XT35 PTH_MACFA</a>	Parathyroid hormone precurs...	85	1e-16
<a href="#">gi 6980561 pdb 1BWV </a>	The Solution Structure Of Human Parat...	85	1e-16 <b>S</b>
<a href="#">gi 209186 gb AAA73011.1 </a>	parathyroid hormone >gi 565142 gb ...	85	1e-16
<a href="#">gi 1942096 pdb 1ZWA </a>	Structure Of Human Parathyroid Hormon...	85	1e-16 <b>S</b>
<a href="#">gi 1065314 pdb 1HPH </a>	Human Parathyroid Hormone Fragment 1 ...	85	1e-16 <b>S</b>
<a href="#">gi 4506267 ref NP_000306.1 </a>	parathyroid hormone preproprote...	85	1e-16 <b>L</b>
<a href="#">gi 1942097 pdb 1ZWB </a>	Structure Of Human Parathyroid Hormon...	83	8e-16 <b>S</b>
<a href="#">gi 131548 sp P01269 PTHY_PIG</a>	PARATHYROID HORMONE PRECURSOR ...	83	8e-16 <b>L</b>
<a href="#">gi 1709894 sp P52212 PTHY_CANFA</a>	PARATHYROID HORMONE PRECURS...	82	1e-15 <b>L</b>
<a href="#">gi 1942099 pdb 1ZWD </a>	Structure Of Human Parathyroid Hormon...	80	6e-15 <b>S</b>
<a href="#">gi 229314 prf 701028A</a>	parathyrin	79	9e-15
<a href="#">gi 1942098 pdb 1ZWC </a>	Structure Of Bovine Parathyroid Hormo...	79	9e-15 <b>S</b>

gi 163647 gb AAA30749.1	preproparathyroid hormone	79	9e-15	L
gi 11119195 gb AAG30545.1	preproparathyroid hormone [Felis...	79	9e-15	
gi 31982386 ref NP_776379.2	parathyroid hormone [Bos tauru...	79	9e-15	L
gi 2624852 pdb 1HTH	The Solution Structure Of Cyclic Huma...	79	9e-15	S
gi 11513553 pdb 1FVY A	Chain A, Solution Structure Of The O...	78	2e-14	S
gi 1942100 pdb 1ZWE	Structure Of Human Parathyroid Hormon...	77	4e-14	S
gi 2392655 pdb 1ZWF	Structure Of N-Terminal Acetylated Hu...	77	4e-14	S
gi 30387856 gb AAP32220.1	hypothalamic parathyroid hormone...	71	2e-12	
gi 8394100 ref NP_058740.1	parathyroid hormone [Rattus nor...	71	2e-12	L
gi 10181174 ref NP_065648.1	parathyroid hormone; parathyro...	65	2e-10	L
gi 2118603 pir  I51851	parathyroid hormone - rat (fragment)...	64	3e-10	
gi 208546 gb AAA72765.1	parathyroid hormone	54	3e-07	
gi 45382055 ref NP_990783.1	thyroid hormone [Gallus gallus...	45	2e-04	L
gi 6578847 gb AAF18100.1	RELISH [Drosophila simulans]	31	3.1	
gi 6578842 gb AAF18095.1	RELISH [Drosophila simulans] >gi ...	31	3.1	
gi 6681203 ref NP_031894.1	dystrophin, muscular dystrophy;...	30	4.1	L
gi 9790306 ref NP_062879.1	nonstructural polyprotein [Ross...	30	4.1	
gi 21230449 ref NP_636366.1	DNA polymerase III epsilon cha...	30	4.1	
gi 14485761 gb AAK63071.1	parathyroid hormone precursor [P...	30	4.1	
gi 34880638 ref XP_229016.2	similar to dystrophin major mu...	30	4.1	L
gi 25121493 ref NP_740679.1	nsP2 protein [Ross River virus]	30	4.1	
gi 130544 sp P13887 POLN_RRVN	Nonstructural polyprotein [Co...	30	4.1	
gi 1169358 sp P11531 DMD_MOUSE	Dystrophin >gi 478748 pir  S...	30	4.1	L
gi 34881930 ref XP_347351.1	similar to dystrophin major mu...	30	4.1	L
gi 15225157 ref NP_180751.1	expressed protein [Arabidopsis...	30	5.5	
gi 27803069 emb CAD60772.1	unnamed protein product [Podosp...	29	7.4	
gi 21226751 ref NP_632673.1	glucosyltransferase [Methanosa...	29	7.4	
gi 21219194 ref NP_624973.1	conserved hypothetical protein...	29	13	
gi 23237772 dbj BAC16514.1	DASK1 [Drosophila melanogaster]	29	13	
gi 46908685 ref YP_015074.1	helicase family protein [Liste...	29	13	
gi 24648284 ref NP_477089.2	CG4720-PA [Drosophila melanoga...	29	13	L
gi 45546033 ref ZP_00186140.1	COG0824: Predicted thioester...	29	13	
gi 15227946 ref NP_181775.1	meprin and TRAF homology domai...	29	13	
gi 33944625 ref XP_340460.1	GTP-binding elongation factor ...	29	13	
gi 32401356 gb AAP80850.1	ATP-binding protein of ABC trans...	29	13	
gi 16804551 ref NP_466036.1	similar to late competence pro...	29	13	
gi 47015567 gb EAL06499.1	competence protein, putative [Li...	29	13	
gi 23471851 ref ZP_00127180.1	COG2120: Uncharacterized pro...	28	18	
gi 8118486 gb AAF72998.1	glutathione-S-transferase [Vibrio...	28	18	
gi 13124709 sp O32513 ENO_DESVM	Enolase (2-phosphoglycerate...	28	18	
gi 33859803 ref NP_796294.1	RIKEN cDNA F730038I15 gene [Mu...	28	18	L
gi 26354546 dbj BAC40901.1	unnamed protein product [Mus mu...	28	18	L
gi 23023912 ref ZP_00063140.1	COG0136: Aspartate-semialdeh...	28	18	
gi 31207383 ref XP_312658.1	ENSANGP00000020654 [Anopheles ...	28	18	
gi 15601256 ref NP_232887.1	glutathione S-transferase, put...	28	18	
gi 33239720 ref NP_874662.1	Isoleucyl-tRNA synthetase [Pro...	28	18	
gi 5532938 gb AAD44944.1	MHC class I heavy chain [Ambystom...	28	18	
gi 40746939 gb EAA66095.1	hypothetical protein AN0222.2 [A...	28	18	
gi 38110793 gb EAA56460.1	hypothetical protein MG06431.4 [...	28	24	
gi 26248475 ref NP_754515.1	Hypothetical sugar kinase yegV...	28	24	
gi 21450297 ref NP_659157.1	UDP-N-acetyl-alpha-D-galactosa...	28	24	L
gi 24113476 ref NP_707986.1	putative kinase [Shigella flex...	28	24	
gi 40786485 ref NP_955425.1	UDP-N-acetyl-alpha-D-galactosa...	28	24	L
gi 38101314 gb EAA48295.1	hypothetical protein MG10554.4 [...	28	24	

<a href="#">gi 21529333 emb CAC79625.2 </a>	UDP-GalNAc:polypeptide N-acetyl...	28	24	<b>L</b>
<a href="#">gi 39753709 gb AAR30402.1 </a>	NADH dehydrogenase subunit F [Ca...	28	24	
<a href="#">gi 5630076 gb AAD45821.1 </a>	N-acetylgalactosaminyltransferase...	28	24	<b>L</b>
<a href="#">gi 22024024 ref NP_523820.2 </a>	CG9889-PA [Drosophila melanoga...	28	24	<b>L</b>
<a href="#">gi 27364478 ref NP_760006.1 </a>	Sun protein [Vibrio vulnificus...	28	24	
<a href="#">gi 15802575 ref NP_288602.1 </a>	putative kinase [Escherichia c...	28	24	
<a href="#">gi 11545801 ref NP_071370.1 </a>	GALNAC-T11 [Homo sapiens] >gi ...	28	24	<b>L</b>
<a href="#">gi 38100969 gb EAA48013.1 </a>	hypothetical protein MG09143.4 [...	28	24	
<a href="#">gi 26352932 dbj BAC40096.1 </a>	unnamed protein product [Mus mu...	28	24	<b>L</b>
<a href="#">gi 38102749 gb EAA49551.1 </a>	hypothetical protein MG08466.4 [...	28	24	
<a href="#">gi 34557142 ref NP_906957.1 </a>	HYDROXY-DEHYDRATASE ACTIVATOR ...	28	24	
<a href="#">gi 37681411 ref NP_936020.1 </a>	sun protein [Vibrio vulnificus...	28	24	
<a href="#">gi 10438776 dbj BAB15338.1 </a>	unnamed protein product [Homo s...	28	24	<b>L</b>
<a href="#">gi 21429970 gb AAM50663.1 </a>	GH20107p [Drosophila melanogaster]	28	24	<b>L</b>
<a href="#">gi 25152947 ref NP_497872.2 </a>	GLYcosylation related, UDP-N-a...	27	32	<b>L</b>
<a href="#">gi 45825856 gb AAS77593.1 </a>	RELISH [Drosophila mauritiana]	27	32	
<a href="#">gi 12842280 dbj BAB25542.1 </a>	unnamed protein product [Mus mu...	27	32	<b>L</b>
<a href="#">gi 45825858 gb AAS77594.1 </a>	RELISH [Drosophila mauritiana]	27	32	
<a href="#">gi 45825866 gb AAS77598.1 </a>	RELISH [Drosophila mauritiana]	27	32	
<a href="#">gi 46488050 gb AAS99367.1 </a>	Relish [Drosophila sechellia]	27	32	
<a href="#">gi 32567074 ref NP_504981.2 </a>	carboxylesterase, type B famil...	27	32	<b>L</b>
<a href="#">gi 34558222 ref NP_908037.1 </a>	hypothetical protein WS1928 [W...	27	32	
<a href="#">gi 45825862 gb AAS77596.1 </a>	RELISH [Drosophila mauritiana]	27	32	
<a href="#">gi 15678500 ref NP_275615.1 </a>	DNA helicase II [Methanothermo...	27	32	
<a href="#">gi 27924341 gb AAH45036.1 </a>	Cg2107-prov protein [Xenopus lae...	27	32	<b>L</b>
<a href="#">gi 27374208 gb AAO00972.1 </a>	Pk92B-PA [Drosophila erecta]	27	32	
<a href="#">gi 38234205 ref NP_939972.1 </a>	Putative asparagine synthetase...	27	32	
<a href="#">gi 45825864 gb AAS77597.1 </a>	RELISH [Drosophila mauritiana]	27	32	
<a href="#">gi 33859650 ref NP_035973.1 </a>	membrane bound C2 domain conta...	27	32	<b>L</b>
<a href="#">gi 8393755 ref NP_058945.1 </a>	membrane bound C2 domain contai...	27	32	<b>L</b>
<a href="#">gi 46135507 ref ZP_00162994.2 </a>	COG0457: FOG: TPR repeat [An...	27	32	
<a href="#">gi 46488052 gb AAS99368.1 </a>	Relish [Drosophila sechellia]	27	32	
<a href="#">gi 46488048 gb AAS99366.1 </a>	Relish [Drosophila sechellia]	27	32	

## Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|7416876|gb|AAF62347.1|](#) parathyroid hormone [Equus caballus]  
Length = 86

Score = 85.5 bits (194), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN  
Sbjct: 3 SVSEIQLMHNLGKHLNSERVEWLRKKLQDVHN 35

☐ >[gi|13124462|sp|Q9XT35|PTH\\_MACFA](#) Parathyroid hormone precursor (Parathyrin) (PTH  
[gi|5359716|gb|AAD42777.1|](#) parathyroid hormone precursor [Macaca fascicularis])

Length = 115

Score = 85.0 bits (193), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 64

☐ >[gi|6980561|pdb|1BWV|](#) **S** The Solution Structure Of Human Parathyroid Hormone Fra  
1-39, Nmr, 10 Structures  
Length = 39

Score = 85.0 bits (193), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

☐ >[gi|209186|gb|AAA73011.1|](#) parathyroid hormone  
[gi|565142|gb|AAB31748.1|](#) human parathyroid hormone; hPTH [synthetic construct]  
Length = 85

Score = 85.0 bits (193), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 2 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 34

☐ >[gi|1942096|pdb|1ZWA|](#) **S** Structure Of Human Parathyroid Hormone Fragment 1-34, N  
Structures

[gi|6980572|pdb|1HPY|](#) **S** The Solution Structure Of Human Parathyroid Hormone Fragm  
In 20% Trifluorethanol, Nmr, 10 Structures

[gi|10120514|pdb|1ET1|A](#) **S** Chain A, Crystal Structure Of Human Parathyroid Hormone  
0.9 A Resolution

[gi|10120515|pdb|1ET1|B](#) **S** Chain B, Crystal Structure Of Human Parathyroid Hormone  
0.9 A Resolution  
Length = 34

Score = 85.0 bits (193), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

☐ >[gi|1065314|pdb|1HPH|](#) **S** Human Parathyroid Hormone Fragment 1 - 37 (Hpth(1-37))  
Structures)



Length = 37

Score = 85.0 bits (193), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 33

☐ >[gi|4506267|ref|NP\\_000306.1|](#) ☐ parathyroid hormone preproprotein; parathyrin; pa sapiens]

[gi|131547|sp|P01270|PTHY\\_HUMAN](#) ☐ Parathyroid hormone precursor (Parathyrin) (PTH)

[gi|2144647|pir||PTHU](#) parathyroid hormone precursor [validated] - human

[gi|37144|emb|CAA23843.1|](#) ☐ unnamed protein product [Homo sapiens]

[gi|190704|gb|AAA60215.1|](#) ☐ preproparathyroid hormone

Length = 115

Score = 85.0 bits (193), Expect = 1e-16

Identities = 29/33 (87%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 32 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 64

☐ >[gi|1942097|pdb|1ZWB|](#) ☐ Structure Of Human Parathyroid Hormone Fragment 2-37, N Structures  
Length = 36

Score = 82.5 bits (187), Expect = 8e-16

Identities = 28/32 (87%), Positives = 28/32 (87%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

VSEIQ HN GKHLNS ERVEWLRKKLQDVHN

Sbjct: 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 32

☐ >[gi|131548|sp|P01269|PTHY\\_PIG](#) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH)  
[gi|2144646|pir||PTPG](#) parathyroid hormone precursor - pig  
[gi|1839|emb|CAA29193.1|](#) ☐ unnamed protein product [Sus scrofa]  
Length = 115

Score = 82.5 bits (187), Expect = 8e-16

Identities = 28/33 (84%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32

SVSEIQ HN GKHL+S ERVEWLRKKLQDVHN

Sbjct: 32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDVHN 64

☐ >[gi|1709894|sp|P52212|PTHY\\_CANFA](#) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH)  
[gi|1085421|pir||JC4202](#) parathyroid hormone precursor - dog

☐ [gi|558916|gb|AAA82584.1|](#) **L** parathyroid hormone precursor  
Length = 115

Score = 81.7 bits (185), Expect = 1e-15  
Identities = 28/33 (84%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
SVSEIQ HN GKHL+S ERVEWLRKKLQDVHN  
Sbjct: 32 SVSEIQFMHNLGKHLSSMERVEWLRKKLQDVHN 64

☐ [>gi|1942099|pdb|1ZWD|](#) **S** Structure Of Human Parathyroid Hormone Fragment 3-37, N  
Structures  
Length = 35

Score = 79.5 bits (180), Expect = 6e-15  
Identities = 27/31 (87%), Positives = 27/31 (87%), Gaps = 1/31 (3%)

Query: 3 SEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
SEIQ HN GKHLNS ERVEWLRKKLQDVHN  
Sbjct: 1 SEIQLMHNLGKHLNSMERVEWLRKKLQDVHN 31

☐ [>gi|229314|prf||701028A](#) parathyrin  
Length = 84

Score = 79.1 bits (179), Expect = 9e-15  
Identities = 27/32 (84%), Positives = 28/32 (87%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL+S ERVEWLRKKLQDVHN  
Sbjct: 2 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHN 33

☐ [>gi|1942098|pdb|1ZWC|](#) **S** Structure Of Bovine Parathyroid Hormone Fragment 1-37,  
Structures  
Length = 37

Score = 79.1 bits (179), Expect = 9e-15  
Identities = 27/32 (84%), Positives = 28/32 (87%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL+S ERVEWLRKKLQDVHN  
Sbjct: 2 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHN 33

☐ [>gi|163647|gb|AAA30749.1|](#) **L** preproparathyroid hormone  
Length = 115

Score = 79.1 bits (179), Expect = 9e-15  
Identities = 27/32 (84%), Positives = 28/32 (87%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL+S ERVEWLRKKLQDVHN

Sbjct: 33 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHN 64

☐ >gi|11119195|gb|AAG30545.1| preproparathyroid hormone [Felis catus]  
Length = 115

Score = 79.1 bits (179), Expect = 9e-15  
Identities = 27/33 (81%), Positives = 29/33 (87%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
SVSEIQ HN GKHL+S ERVEWLR+KLQDVHN  
Sbjct: 32 SVSEIQFMHNLGKHLSSVERVEWLRKKLQDVHN 64

☐ >gi|31982386|ref|NP\_776379.2| ☒ L parathyroid hormone [Bos taurus]  
gi|131545|sp|P01268|PTHY\_BOVIN Parathyroid hormone precursor (Parathyrin) (PTH)  
gi|69233|pir||PTBO parathyroid hormone precursor - bovine  
gi|85|emb|CAA23439.1| ☒ L preproparathyroid hormone [Bos taurus]  
gi|163643|gb|AAA30747.1| ☒ L preproparathyroid hormone  
gi|163645|gb|AAA30748.1| ☒ L preproparathyroid hormone  
Length = 115

Score = 79.1 bits (179), Expect = 9e-15  
Identities = 27/32 (84%), Positives = 28/32 (87%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL+S ERVEWLRKKLQDVHN  
Sbjct: 33 VSEIQFMHNLGKHLSSMERVEWLRKKLQDVHN 64

☐ >gi|2624852|pdb|1HTH| ☒ S The Solution Structure Of Cyclic Human Parathyroid Horm  
Fragment 1 - 34, Nmr, 10 Structures  
Length = 34

Score = 79.1 bits (179), Expect = 9e-15  
Identities = 27/33 (81%), Positives = 27/33 (81%), Gaps = 1/33 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
SVSEIQ HN G HLN ERVEWLRKKLQDVHN  
Sbjct: 1 SVSEIQLXHNLGXHLNEXERVEWLRKKLQDVHN 33

☐ >gi|11513553|pdb|1FVY|A ☒ S Chain A, Solution Structure Of The Osteogenic 1-31 Fra  
The Human Parathyroid Hormone  
Length = 31

Score = 77.8 bits (176), Expect = 2e-14  
Identities = 27/31 (87%), Positives = 27/31 (87%), Gaps = 1/31 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDV 30  
SVSEIQ HN GKHLNS ERVEWLRKKLQDV  
Sbjct: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

☐ >[gi|1942100|pdb|1ZWE|](#) **S** Structure Of Human Parathyroid Hormone Fragment 4-37, N  
Structures  
Length = 34

Score = 77.0 bits (174), Expect = 4e-14  
Identities = 26/30 (86%), Positives = 26/30 (86%), Gaps = 1/30 (3%)

Query: 4 EIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
EIQ HN GKHLNS ERVEWLRKKLQDVHN  
Sbjct: 1 EIQLMHNLGKHLNSMERVEWLRKKLQDVHN 30

☐ >[gi|2392655|pdb|1ZWFI|](#) **S** Structure Of N-Terminal Acetylated Human Parathyroid Ho  
Nmr, 10 Structures  
[gi|2392656|pdb|1ZWI|](#) **S** Succinyl Human Parathyroid Hormone 4-37, Nmr, 10 Structur  
Length = 35

Score = 77.0 bits (174), Expect = 4e-14  
Identities = 26/30 (86%), Positives = 26/30 (86%), Gaps = 1/30 (3%)

Query: 4 EIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
EIQ HN GKHLNS ERVEWLRKKLQDVHN  
Sbjct: 2 EIQLMHNLGKHLNSMERVEWLRKKLQDVHN 31

☐ >[gi|30387856|gb|AAP32220.1|](#) hypothalamic parathyroid hormone [Rattus sp.]  
Length = 105

Score = 71.5 bits (161), Expect = 2e-12  
Identities = 25/32 (78%), Positives = 27/32 (84%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL S ER++WLRKKLQDVHN  
Sbjct: 23 VSEIQLMHNLGKHLASVERMQWLRKKLQDVHN 54

☐ >[gi|8394100|ref|NP\\_058740.1|](#) **L** parathyroid hormone [Rattus norvegicus]  
[gi|131549|sp|P04089|PTHY\\_RAT](#) **L** Parathyroid hormone precursor (Parathyrin) (PTH)  
[gi|92588|pir||A05091](#) parathyroid hormone precursor - rat  
[gi|56003|emb|CAA29192.1|](#) **L** unnamed protein product [Rattus norvegicus]  
[gi|206485|gb|AAA41979.1|](#) **L** preproparathyroid hormone  
Length = 115

Score = 71.5 bits (161), Expect = 2e-12  
Identities = 25/32 (78%), Positives = 27/32 (84%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL S ER++WLRKKLQDVHN  
Sbjct: 33 VSEIQLMHNLGKHLASVERMQWLRKKLQDVHN 64

☐ >[gi|10181174|ref|NP\\_065648.1|](#) **L** parathyroid hormone; parathyroid hormone precurs

gi|4092930|gb|AAC99656.1| **L** parathyroid hormone precursor [Mus musculus]  
Length = 115

Score = 64.7 bits (145), Expect = 2e-10  
Identities = 23/32 (71%), Positives = 27/32 (84%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
VSEIQ HN GKHL S ER++WLR+KLQD+HN  
Sbjct: 33 VSEIQLMHNLGKHLASMERMQWLRRLKQLDMHN 64

gi|2118603|pir||I51851 parathyroid hormone - rat (fragment)  
gi|601933|gb|AAA57156.1| parathyroid hormone precursor [Rattus norvegicus]  
Length = 105

Score = 64.3 bits (144), Expect = 3e-10  
Identities = 23/32 (71%), Positives = 26/32 (81%), Gaps = 1/32 (3%)

Query: 2 VSEIQ-AHNAGKHLNSNERVEWLRKKLQDVHN 32  
+SEIQ HN GKHL S ER++WLRKKLQD HN  
Sbjct: 23 ISEIQLMHNLGKHLASVERMQWLRKKLQDGHN 54

gi|208546|gb|AAA72765.1| parathyroid hormone  
Length = 67

Score = 54.1 bits (120), Expect = 3e-07  
Identities = 15/15 (100%), Positives = 15/15 (100%)

Query: 18 ERVEWLRKKLQDVHN 32  
ERVEWLRKKLQDVHN  
Sbjct: 2 ERVEWLRKKLQDVHN 16

gi|45382055|ref|NP\_990783.1| **L** thyroid hormone [Gallus gallus]  
gi|131546|sp|P15743|PTHY\_CHICK PARATHYROID HORMONE PRECURSOR (PTH)  
gi|86411|pir||A34937 parathyroid hormone precursor - chicken  
gi|212592|gb|AAB02866.1| **L** parathyroid hormone precursor [Gallus gallus]  
gi|212768|gb|AAA49093.1| **L** thyroid hormone precursor  
Length = 119

Score = 44.8 bits (98), Expect = 2e-04  
Identities = 19/32 (59%), Positives = 25/32 (78%), Gaps = 1/32 (3%)

Query: 1 SVSEIQ-AHNAGKHLNSNERVEWLRKKLQDVH 31  
SVSE+Q HN G+H ++ ER +WL+ KLQDVH  
Sbjct: 32 SVSEMQLMHNLGHRHTVERQDWLQMKLQDVH 63

gi|6578847|gb|AAF18100.1| RELISH [Drosophila simulans]  
Length = 817

Score = 30.8 bits (65), Expect = 3.1  
Identities = 14/28 (50%), Positives = 16/28 (57%), Gaps = 8/28 (28%)